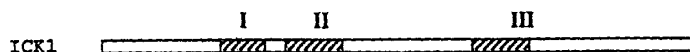


09/733507

A



B

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M V 2

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R K Y R K A G I V E A G V S S T Y M Q 22

CTACGGAGCGGAGAATTGTTTATGTTAGATCGGAAAAATCAAGCTCTGTCTCCGTCGTC 180  
L R S R R I V Y V R S E K S S S V S V V 42

GGTGATAATGGAGTTTCGTCGTCTTGTAGTGAAGCAATGAATATAAGAAGAAAGAATTA 240  
G D N G V S S S C S G S N E Y K K K E L 62

VI VII  
ATACATCTGGAGGAGGAAGATAAAGATGGTGACACTGAAACGTCGACGTATCGACGGGT 300  
I H L E E E D K D G D T E T S T Y R R G 82

ACGAAGAGGAAGCTTTTGAATCTGAGAGAGGAGGAGAAAGAAGAAATTAAGTAAATCC 360  
T K R K L F E N L R E E E K E E L S K S 102

ATGGAGAATTATTCATCGGAATTGAATCGGCGGTTAAAGAATCGTTAGATTGTTGTTGT 420  
M E N Y S S E F E S A V K E S L D C C C 122

AGCGGGAGGAAAACGATGGAGGAGACGGTGACGGCGGAGGAGGAGGAGAAGGCCGAAATTG 480  
S G R K T M E E T V T A E E E E K A K L 142

ATGACGGAGATGCCAACGGAATCGGAAATTGAAGATTTTTTGTGGAAGCTGAGAAACAA 540  
M T E M P T E S E I E D F F V E A E K Q 162

VIII  
CTCAAAGAAAATTCAAGAAGTACAATTCGATTTCGAGAAGGAGAAGCCATTAGAA 600  
L K E K F K K K Y N F D F E K E K P L E 182

GGACGTTACGAATGGGTAAAGTTAGAGTGAAGAAGAAGAAGTTTATGGTTTTTTTTT 660  
G R Y E W V K L E . 191

TAACTTTTTAGATTTTAATATTTTCAGGGAATAAGTTAATTTTATTTTGTGATTGGAAA 720

TATAAGATTGTAGGAGGAATGTTTTTGAAGTACGAAATTGCACAGAAAAGAAGAAAG 780

CTTTTAAACAGATTTTAGAGCCCAGAAAAGTCGTGCTTTTAGCTCTACTTTTACCTCTT 840

CTTCGAATCTTGTGTATCTTTTAGCATATCTTTAGTACAATTTTATGTTTTTGGTGAAT 900  
GATA\* 905

Characterization of cDNA (Wang et al., 1997) and genomic sequences of *ICK1*.  
(A). Genomic organization *ICK1*. Open bars represent exons and filled bars, introns.  
(B). Features of cDNA sequence and deduced amino acid sequence.

Figure 1

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8

61 ACGTATATGCAGCTACGGAGCCGGAGAAATTGTTTATGTTAGATCGGAAAAATCAAGCTCT Ick1.seq  
 3 ACGTATATGCAGCTACGGAGCCGGAGAAATTGTTTATGTTAGATCGGAAAAATCAAGCTCT ICK1b.seq  
 6 [REDACTED] GATTTTT [REDACTED] TAG [REDACTED] ICK1c.seq

121 GTCTCCGTCGTCGGTGATAATGGAGTTTCGTCGCTTGTAGTGAAGCAATGAATATAAG Ick1.seq  
 63 GTCTCCGTCGTCGGTGATAATGGAG [REDACTED] ICK1b.seq  
 18 [REDACTED] ICK1c.seq

181 AAGAAAGAATTAATACATCTGGAGGAGGAAGATAAAGATGGTGACACTGAAACGTCGACG Ick1.seq  
 88 [REDACTED] ICK1b.seq  
 18 [REDACTED] ICK1c.seq

241 TATCGACGGGGTACGAAGAGGAAGCTTTTTGAAAATCTGAGAGAGGAGGAGAAAGAAGAA Ick1.seq  
 88 [REDACTED] ICK1b.seq  
 18 [REDACTED] GGGTACGAAGAGGAAGCTTTTTGAAAATCTGAGAGAGGAGGAGAAAGAAGAA ICK1c.seq

301 TTAAGTAAATCCATGGAGAATTATTCATCGGAATTTGAATCGGCGGTTAAAGAATCGTTA Ick1.seq  
 88 [REDACTED] AATTATTCATCGGAATTTGAATCGGCGGTTAAAGAATCGTTA ICK1b.seq  
 70 TTAAGTAAATCCATGGAGAATTATTCATCGGAATTTGAATCGGCGGTTAAAGAATCGTTA ICK1c.seq

361 GATTGTTGTTGTAGCGGGAGGAAAACGATGGAGGAGACGGTGACGGCGGAGGAGGAGGAG Ick1.seq  
 130 GATTGTTGTTGTAGCGGGAGGAAAACGATGGAGGAGACGGTGACGGCGGAGGAGGAGGAG ICK1b.seq  
 130 GATTGTTGTTGTAGCGGGAGGAAAACGATGGAGGAG [REDACTED] GAGGAG ICK1c.seq

421 AAGGCGAAATTGATGACGGAGATGCCAACGGAATCGGAAATTGAAGATTTTTTTGTGGAA Ick1.seq  
 190 AAGGCGAAATTGATGACGGAGATGCCAACGGAATCGGAAATTGAAGATTTTTTTGTGGAA ICK1b.seq  
 172 AAGGCGAAATTGATGACGGAGATGCCAACGGAATCGGAAATTGAAGATTTTTTTGTGGAA ICK1c.seq

461 GCTGAGAAACAACTCAAAGAAAAATTCAAGAAGAAGTACAATTTTCGATTTTCGAGAAGGAG Ick1.seq  
 250 GCTGAGAAACAACTCAAAGAAAAATTCAAGAAGAAGTACAATTTTCGATTTTCGAGAAGGAG ICK1b.seq  
 232 GCTGAGAAACAACTCAAAGAAAAATTCAAGAAGAAGTACAATTTTCGATTTTCGAGAAGGAG ICK1c.seq

541 AAGCCATTAGAAGGACGTTACGAATGGGTAAAGTTAGAGTGAAGAAGAAGAAGATTTA Ick1.seq  
 310 AAGCCATTAGAAGGACGTTACGAATGGGTAAAGTTAGAGTGAAGAAGAAGAAGATTTA ICK1b.seq  
 292 AAGCCATTAGAAGGACGTTACGAATGGGTAAAGTTAGAGTGAAGAAGAAGAAGATTTA ICK1c.seq

601 TGGTTTTTTTTTAACTTTTTAGATTTTAATATTTAGGGAATAAGTTAATTTTATTTTG Ick1.seq  
 370 TGGTTTTTTTTTAACTTTTTAGATTTTAATATTTAGGGAATAAGTTAATTTTATTTTG ICK1b.seq  
 352 TGGTTTTTTTTTAACTTTTTAGATTTT ICK1c.seq

661 TTGATTTGGAAATATAAGATTGTAGGAGGAATGTTTTAGAAAGTACGAAATTGCACAGA Ick1.seq  
 430 TTGATTTGGAAATATA ICK1b.seq  
 379 ICK1c.seq

Alignment of *ICK1* cDNA sequence with *ICK1b* and *ICK1c* showing the differences

Figure 2

GTGGAATCTAGGATAATTCTGTCTCCGTGTGTACAGGCGACGAATCGCGGTGGAATTGTG  
GCGAGAAATTCAGCAGGAGCGTCGGAGACGAGTGTGTTATAGTACGACGGCGAGATTCT  
CCTCCGGTTGAAGAACAGTGTCAAATCGAAGAAGAAGATTCGTCGGTTTCGTGTTGTTCT  
ACATCGGAAGAGAAATCGAAACGGAGAATCGAATTTGTAGATCTTGAGGAAAATAACGGT  
GACGATCGTGAACAGAAACGTCGTGGATTACGATGATTTGAATAAGAGTGAGGAATCG  
ATGAACATGGATTCTTCTTCGGTGGCTGTTGAAGATGTAGAGTCTCGCCGCAGGTTAAGG  
AAGAGTCTCCATGAGACGGTGAAGGAAGCTGAGTTAGAAGACTTTTTTCAGGTGGCGGAG  
AAAGATCTTCGGAATAAGTTGTTGGAATGTTCTATGAAGTATAACTTCGATTTTCGAGAAA  
GATGAGCCACTTGGTGGAGGAAGATACGAGTGGGTAAATTGAATCCATGAAGAAGACGA  
TGATGATAATGATGATCATTTGTTTTCAACAAAGTACTTATTATTTCTTCTCTGTAATAAT  
CTTTGCTTTGATTTTTCTTTTAACAAAATCCAAATGTAGATATCTTTCTCTCGAATAATC  
AATAACATGTAATTCAACTTTTGTGTTGTTACTTCCTTGAGGTAATTAATTAGATTCGTGTT  
TTTCTCGATTAATAAACTATAAGTTTATAACTAAA

cDNA sequence of *ICK2*

Figure 3

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SUBSTITUTE SHEET (RULE 26)

AAAAAAAAAGCAGAGAGAGAGAGCACACAAAAATCCAAGAGAGAAAAAATGAGCGAGAGA  
AAGCGAGAGCTTGCAGAAGAAGCTTCAAGCACAAAGCTTCTCACCCTGAAGAAAACGAAG  
CTTAATGATTCTTCTGATTATCACCAGGACTCTCATGACGTCATCGTCTTCGCGGTTTCA  
TCTTCTTCCGTTGCTTCGTTCGGCGGCTTTAGCGTCTGATGAATGTTCCGTTACCATCGGT  
GGAGAAGAAAGTGATCAGTCCTCGAGTATCAGCTCCGGTTGTTTCACCAGTGAATCGAAA  
GAAATCGCGAAGAACAGTTCGTTCGTTTGGTGTAGATCTGGAGGATCATCAAATCGAAACC  
GAAACCGAAACCTCAACATTATCACCAGCAATTTAGAAAAGAGACGAGTCCAGTGAGT  
GAGGGTTTGGGAGAAACGACAACAGAAATGGAATCATCATCGGCAACGAGAGAAAACAA  
CCGGGGGTGAGGAAGACTCCAACGGCGGGGAGATTGAGGATTTGTTCTCGGAGCTAGAG  
AGTCAAGACGATAAGAAGAAGCAATTCATAGAAAAGTACAACCTCGATATTGTCAATGAC  
GAACCGCTTGAAGGTCGCTACAAGTGGGATCGACTTTAAGCCATCAAAAAGCAAATACCA  
TCCATGAAGAAGACAAAAGAAAAATAGGTTTTGTTTTTCGTGGTTAACATTTCCACTTGT  
ACAGCTCTAGTCTATTTCTCTTTAAAAACCTATGTTACTAGTTCGTACAAAACAAAACAA  
AAAACACGACCTTTATAATGAAATTTCCGATCTTGGCTACTAAA

cDNA sequence of *ICN2*

Figure 4

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SUBSTITUTE SHEET (RULE 26)

008021 055E/60

CTCTCTCCAGAGAAAACCTATAATGAGCTTGAGAGAAATGAGCGAAACAAACCCAGAGA  
GATTCTGAGTACGAAGGATCAAAACATCAAGAGGATGAGACTCGATGATGATGATGACGTT  
TTACGCTCACCAGCAGAGAACTCTTCTTCTTCTTCTTCTTCTCTGCGTTACTCGGTT  
TCAGATCTCCGAGGTTTCTGCTCCGTCGCGTTATCTGAAGAAGAACGATCATTAAGC  
TCAAGCATCAGCTCTGGTTGTTCCAGCAGCGAAACTAACGAATCGCTACTCGTCTTCCA  
TTTTCAGATCTGGAGGCTCATGAAATCTCCGAAACCGAAATCTCAACGTTACTCACCAC  
AATTTCAGGAAACAGGGAATTTATCAAGCAGAAATCTGGGAGAAACAGCAGAAATGGAC  
TCGGCCAGCAGCGGATGAGAGATCAGAGAAACGCGGAGAGAAGAGAAGATGGA  
TACCAGCGCAGGCGAGAGCTTGATGACTTTTCTCGCGCGCAGGAGATACGAACAGAA  
CGATTCACAGAAAAGTACAACATACGACATCGTCAATGATACGCGCGTTGAAGGTCGGTAC  
CAGTGGGTTAGTCTGAAACCTTAGAAGCCATGGAAGAACAAA

### cDNA sequence of ICN6

[illegible]

Figure 5

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ATTAAAGAGTCTGGTCCAGGTCTCGCGTTGACTCGGTAACTCGGCTCCTGTAGCTCAG  
 AGCTCTAATGAAGATGAATGTTTTGACAATTTCTGTAGTGTCCAAGTTCTTGTGGTGAA  
 AACAGTCTCGGTTTTGAATCAAGACACAGCACAAGGGAGAGCACGCCTTGTAACCTTGT  
 GAGGATATGGAGATCATGGTTACACCAAGGTCTAGCACGAGGTCGATGTGCAGAGCAACC  
 AAAGAGTACACAAGGGAACAAGATAACGTGATCCCGACCACTAGTGAAATGGAGGAGTTC  
 TTTGCATATGCAGAGCAGCAGCAACAGAGGCTATTTCATGGAGAAGTACAACCTCGACATT  
 GTGAATGATATCCCCCTCAGCGGACGTTACGAATGGGTGCAAGTCAAACCATGAAGTTCA  
 AAAGGAAACAGCTCCAAAAGACATGGTGTGAAGTTAGAGAATTGTGATGGAGTTTAACAG  
 AACTAACCAACATCAGAAATCGTGTAAATCCTTAAGTTAATAATGTGGGTTA

**cDNA sequence of ICN7**

**SEQ ID NO. 15: The nucleotide sequence of *Chenopodium rubrum* CDKII  
 (GenBank AJ002173)**

gcacgagcgaaattgcggtgtaggaggttaaaccagagctcgagactgccctagctatggcggcagctgctactccaac  
 ttcgtctccggcgaagaagatcaagaaggttcgaagtcgtcgataatattcctcaactaagaagtcgtcgaaagaatt  
 tgcggcgccggagaatttcgccgaattagaacgacgccgttggaagttgcggcggttgtaggaggaagaggttgcg  
 aattgctcagtagcaggttaattactacagctaggtcggattttccgccgtcttctgctcaagcaattatgatcagtt  
 gagtttagcagagccagaagtagttaaggatgatgatggttgggaatcgtacagcagatccagaggttgagagtggtg  
 aggcgtcgtcaagcaaaaggagagccatagaacagaagcgagagaagctacaaaattagacgaccaggattatccggcg  
 acgaaatcaacgggtacagatcaagatgccgtctgattcagaatcgaagaattcttctgttctgtaaaaagatccca  
 gaaacgcttcagcgaaaagtacaatttcgacatagtaaggacgtgccactgaaggtcggtatgattgggttccaataa  
 atccatgaataaaacccactggtgatagtgatgatgaatgactgaattctccacaattacgcaaaattagccact  
 gaaattgcaagtaaatcttaatttagcctttcttcttttagcagaagttgatctattctcacaccgaaaaaaaa  
 aaaa

**SEQ ID NO. 16: The amino acid sequence of *Chenopodium rubrum* CDKII**  
 MAAAATPTSS PAKKIKK VSK SSYNIPQLRS RRKNLSAPEN FAELETTPL  
 VAAVVEEEVANCSSSEVIT TARSDFPSC CSSNYDQLSS SEPEVVKDDD  
 GLGNRTADPE VESGEASSKQ KESHRTEARE ATKLDDQDYP ATKSTVQIKM  
 PSDSEIEEFF AVAEKDLQKR FSEKYNFDIV KDVPLKGRYD WVPINP

Figure 6

0000021 2055E260

```

.....S.....V...S...SV...S.S.....C.....E.....S.S Consensus
1  MVRKYRKA-----KGIVEAGVSYTMQLRRIV-----YVRSEKSSSVGVNDCSSCGSGNEYKKELIHLFEEDKGDG ICK1.pro
1  V-----ESRIILSPCVQATNRGGIVARNRAGA-----SETSVIVRRRDPVPV-----EEQ-----QIIEEDSV ICK2.pro
1  KKKQERAHKNPREKKMSERKRELAEASTSFSLPKTKLNDSSDSDSPDSDHVI FAVSSSSASAAALASDESVTIGGSDQ--S ICN2.pro
1  LS--PEKTIIMSLREMSKPKRDSEYEGN-----IKRMLDDDDVLRSPTRLIS--SSSSLAYVDSGGFSSVALSEEDDHLIS ICN6.pro
1  IKESGSRSRVD-----VNVLPVAQSNEDEFDNFV----- ICN7.pro

.....C...SE.K-----F.DLE.....E.....F.K.....E.L.E.....S.....R.....K.K.....PT.AE.E Consensus
74  TETSTYRRGT-----RKLCENRREEKEELSKSMENYSSE-----ESAVKSDCCSGRKTMEETV-TAEEDSALMTMEES ICK1.pro
58  ---CSTEE-----SKRRIE-----VNNNGDDRETETSWIYDDLNSSESM--NMDSSVAVEDVESRR-----LRSLHETVKE ICK2.pro
90  ISSGFTSSS EIAKNSSSGVSDHQIETETSTFITSNETSPVSGGCTTTEMESSATK-----QPGVRKT ICK2.pro
83  ISSGSSSTNEIATRLP-S-----AHEI-S TEISTLLTNPRQGSSSSNGTA-EMDATTEDQKTEKKMEKSQOLD ICN6.pro
34  VQVSSGEN-----SLGF SRHSTRSTPCNFV-----DM-IMVTPGSTSRMCRATKEYTREQDNVITSM ICN7.pro

DFF..AE.-.Q....F.E---KYNFDIVND.PLEG-RYEWV.L.P- Consensus
154  VEK--LKEKKK-----FEKEK-----KE ICK1.pro
134  QVAK--DLRNKLLCSM-----FEKEK-----GCKKN ICK2.pro
174  LSELQSDDKKKQI-----YVNE-----EKK-----DRL ICN2.pro
169  SARYEKKR-----YVNE-----QSK ICN6.pro
99  EAYE--QQRLM-----YVNE-----QVK ICN7.pro

```

Consensus 'Consensus #1': When 60% (3) match the residue of the Consensus show the residue of the Consensus, otherwise show '.'.  
 Decoration 'Decoration #1': Shade (with black at 40% fill) residues that match the consensus named 'Consensus #1' exactly.

Alignment of deduced amino acid sequences of ICK1, ICK2, ICN2, ICN6 and ICN7

Figure 7

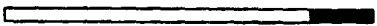
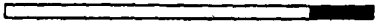
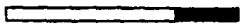
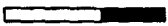

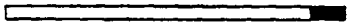
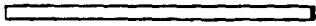
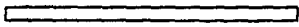
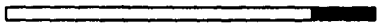
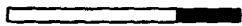
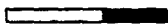





| <u>Bait</u> | <u>ICK1 (Numbers indicate the amino acid positions)</u> | <u>Filter assay</u>   | <u>Activity</u> |
|-------------|---|---|-----------------|
| cdc2a       | /   |   | 0.0             |
| /           | (3-191)   |    | 0.0             |
| cdc2a       | (3-191)   |    | 12.4            |
| cdc2a       | (73-191)  |    | 40.6            |
| cdc2a       | (109-191)   |    | 42.6            |
| cdc2a       | (154-191)   |    | 10.7            |
| cdc2a       | (3-175)   |    | 0.3             |
| cdc2a       | (3-162)   |  | 0.3             |
| cdc2a       | (3-152)   |  | 0.0             |
| cyclin δ3   | /   |   | 0.8             |
| cyclin δ3   | (3-191)   |  | 100.0           |
| cyclin δ3   | (73-191)  |  | 397.3           |
| cyclin δ3   | (109-191)   |  | 480.7           |
| cyclin δ3   | (154-191)   |  | 7.1             |
| cyclin δ3   | (3-175)   |  | 19.9            |
| cyclin δ3   | (3-162)   |  | 2.5             |
| cyclin δ3   | (3-152)   |  | 2.2             |
| ATMPK2      | (3-191)   |  | 0.0             |

Figure 8